

In the Specification:

Replace the alignment starting on page 10, line 14 with the following alignment.

gi|547724 INTERFERON ALPHA PRECURSOR (IFN-ALPHA) (SEQ ID NO:11)
gi|585317 INTERFERON DELTA-1 PRECURSOR (SEQ ID NO:12)
gi|124502 INTERFERON OMEGA-2 PRECURSOR (INTERFERON ALPHA-II-2) (SEQ ID NO:13)
gi|400061 INTERFERON OMEGA-1 PRECURSOR (INTERFERON ALPHA-II-1) (SEQ ID NO:14)

NOV1a
gi|547724 INTERFERON AS
gi|585317 INTERFERON DE
gi|124502 INTERFERON OM
gi|400061 INTERFERON OM
Consensus

10 20 30 40 50 60

NOV1a
gi|547724 INTERFERON AS
gi|585317 INTERFERON DE
gi|124502 INTERFERON OM
gi|400061 INTERFERON OM
Consensus

70 80 90 100 110

NOV1a
gi|547724 INTERFERON AS
gi|585317 INTERFERON DE
gi|124502 INTERFERON OM
gi|400061 INTERFERON OM
Consensus

Replace the alignment starting on page 11, line 8 with the following alignment.

gi|3318960|pdb|1AU1|A Chain A, Human Interferon-Beta Crystal Structure (SEQ ID NO:16)
gi|2624437|pdb|1RH2|A Chain A, Recombinant Human Interferon-Alpha 2b (SEQ ID NO:17)
gi|124432 INTERFERON ALPHA-1 PRECURSOR (SEQ ID NO:18)
gi|2147609 interferon-omega20 - rabbit (SEQ ID NO:19)
Consensus (SEQ ID NO:20)

NOV1a
gi|3318960|pdb|
gi|2624437|pdb|
gi|124432 INTER
gi|2147609 inte
Consensus

10 20 30 40 50 60

NOV1a
gi|3318960|pdb|
gi|2624437|pdb|
gi|124432 INTER
gi|2147609 inte
Consensus

70 80 90 100 110

NOV1a
gi|3318960|pdb|
gi|2624437|pdb|
gi|124432 INTER
gi|2147609 inte
Consensus

Amend the paragraph starting on page 20, line 12 as follows.

D3
This same alignment between KIAA1246 (SEQ ID NO:27) and NOV2 (identified as AF038458A) is shown below.

Replace the alignment starting on page 21, line 1 with the following alignment.

D4

```
KIAA_predicted  --METLLGGLLAFQMA-----FAVVDACPKYCVCONLSESLGTLCPSKGLLFVPPDIDRR
AF038458_A      MATLPLLLCLLPLAPASSFPQSATPSPCFRRRCRCOTQLPLSVLCFPGAGLLFVFPFLDRR

KIAA_predicted  TVELRLGGNFIIHISQDFANMTGLVDLTLSRNTISHIQPFSFLDLLESLSLHLDNSRLP
RICK_AF038458_A AAEELRLADNFIAVRRERLANMTGLHLSLSRNTIRHYAAGAFADLRALRALHLDGNRLT

KIAA_predicted  SLGEDTLRGLVNLQHLIVNNNQLCGLDEAFEDFLLTLEDLDLSYNNLHGLPWDVSUREMV
AF038458_A      SLGEGQLRGLVNLRLHILSNNQLAALAGALDDCAETLEDLDLSYNNLEQLPWEALGELG

KIAA_predicted  NTHQLSLDHNLLDHIAEGTFADLQKLARLDLTSNRLOKLPEDPFFARSQASALTATPFAP
AF038458_A      NVTNLGLDHNLLASVPAGAFSRLHKLARLDMTSNRETTLPEDPFLSELPLLARPRGSPAS

KIAA_predicted  PLSFSFGGNPLHCNCELWLRRLEEDDLETGSGGGLKGRYFWHVREEEFVCEPFLITQ
AF038458_A      ALVLAFGGNPLHCNCELWLRRLEAEDDLEACSEPALGGRYFWAVGEEEFVCEPFLVTH

KIAA_predicted  HTHKLWLLEQAATLCKKANGDPSFLTHWVAFDDRIVNSSRTAVYDNGTLDIFETTSQD
AF038458_A      RSPPLAW'AGRPAALRCRAVGDPEERVRWWSFQGRLLDSSSARAEPNGTLELLVTEPGD

KIAA_predicted  SCAFTCIAANAAGEATAMVEVSLVQLF--HLSNSTSRTAPPKSRLSDITGSSKTSRCGGG
AF038458_A      GGIFTCIAANAAGEATAAVELTVGPPPPFQLANSTSCDPP---RDGDPDALTPPSAASAS

KIAA_predicted  SGGGEPPESEPERAVLVSEVTTTSALWKWSVSKSAPRVKMYQLQYNCSDDDEVLYYRMIPA
AF038458_A      AKVADTG-PETDEGVQVTEHGATAALVQWPDQRPFGGRMYQLQYNSSADDLYYRMIPA

KIAA_predicted  SNKAFVNNLVSGTGVDLCVLAMWDDTATTLTATNIVGCAQFFTKADYPQCQSMHSQILG
AF038458_A      ESRSFLLTDLASGRTYDLCVLAVYEDSATGLTATRPVCCARESTEPALRPCGAPHAPFLG

KIAA_predicted  CTMILVIGGIVATLLVLFIVLLMVRYKWCNHEAF--SKMAAAVSNWYSQTNGAQPPFPSS
AF038458_A      CTMILATGGIVASVLVLFIVLLMVRYKWHGGQPPGKAKTPAPVSSVCSQTNGALGFTPT-

KIAA_predicted  APAGAPPQGPVKVVRNELLDFTASLARASDSSSSSSSLGSGEAAAGLGRAPWRIPPSAPRF
AF038458_A      ---PAPPAPF-----AA-----LRAHTVVLDCPEWGP GHEPVGP

KIAA_predicted  KPSLDRLMGAFASLDLKSQRKEELDSRTFAGRGAGTSARGHHSREPLLGPFAARARSL
AF038458_A      -----

KIAA_predicted  LPLPLEGKAKRSHSFDMGDFAAAAAGGVVPGGYSPPRKVSNIWTKRSLSVNGMLLPFEES
AF038458_A      -----

KIAA_predicted  DLVGARGTFGSSEWVMESTV
AF038458_A      -----
```

Please replace the current sequence listing with the one enclosed.